

SEQUENCE LISTING

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<110> Wei et al.

<120> Human Hematopoietic - Specific Protein

<130> PF268D1C1

<150> PCT/US96/04930
<151> 1996-04-11

<150> 08/837,029
<151> 1997-04-11

<150> 09/265,977
<151> 1999-03-11

<160> 8

<170> PatentIn version 3.1

<210> 1
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<212> DNA
<213> human

<220>
<221> CDS
<222> (42)..(608)
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ctcaaccaca gactacactt gctgaactgg ctccctggggc c atg agg ctg tca ctg      56
                                         Met Arg Leu Ser Leu
                                         -20
cca ctg ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc      104
Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu
-15 -10 -5
ggg gac agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag      152
Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu
-1 1 5 10 15
gag atg tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc      200
Glu Met Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys
20 25 30
aga gct gtg gct tac cag atg tgg caa aat ctg gca aag gca gag acc      248

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[illegible]

<210>	2
<211>	189
<212>	PRT
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<400>      2
Met  Arg  Leu  Ser  Leu  Pro  Leu  Leu  Leu  Leu  Leu  Leu  Gly  Ala  Trp  Ala
      -20                      -15                      -10

Ile  Pro  Gly  Gly  Leu  Gly  Asp  Arg  Ala  Pro  Leu  Thr  Ala  Thr  Ala  Pro
      -5                      -1  1                      5                      10

Gln  Leu  Asp  Asp  Glu  Glu  Met  Tyr  Ser  Ala  His  Met  Pro  Ala  His  Leu
      15                      20                      25

Arg  Cys  Asp  Ala  Cys  Arg  Ala  Val  Ala  Tyr  Gln  Met  Trp  Gln  Asn  Leu
      30                      35                      40

Ala  Lys  Ala  Glu  Thr  Lys  Leu  His  Thr  Ser  Asn  Ser  Gly  Gly  Arg  Arg
      45                      50                      55

Glu  Leu  Ser  Glu  Leu  Val  Tyr  Thr  Asp  Val  Leu  Asp  Arg  Asn  Cys  Ser
      60                      65                      70

Arg  Asn  Trp  Gln  Asp  Tyr  Gly  Val  Arg  Glu  Val  Asp  Gln  Val  Lys  Arg
      75                      80                      85                      90

Leu  Thr  Gly  Pro  Gly  Leu  Ser  Glu  Gly  Pro  Glu  Pro  Ser  Ile  Ser  Val

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95

100

105

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 110 115 120

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
 125 130 135

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
 140 145 150

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
 155 160 165

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer containing a Bam HI restriction site encoding a start AUG, followed by 19 nucleotides of the hHSP coding sequence beginning with the first base of the 23rd codon.

<400> 3

cgcggatccg acagggcgcc actcacag

28

<210> 4

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer containing an Xba I restriction site followed by 21 nucleotides complementary to the last 21 nucleotides of hHSP including the stop codon.

<400> 4

gcgtctagag aggtcactgg gttttatttg

30

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer containing a Bam HI restriction site followed by 19 bases of the sequence of hHSP.

<400> 5

cgcggatccg ccatcatgag gctgtcactg ccac

34

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer containing an Xba I restriction site

followed by nucleotides complementary to the last 21 nucleotides of hHSP including the stop codon.

<400> 6
gcgtctagag aggtcactgg gttttatttg

30

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing a Bam HI site, an AUG start codon and 16 nucleotides thereafter.

<400> 7
cgcccatcgg ccatcatgag gctgtcactg ccac

34

<210> 8
<211> 57
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing an Xba I site, a stop codon, 9 codons forming hemagglutinin tag and 18 bp of 3' coding sequence.

<400> 8
cgctctagat caagcgtagt ctgggacgtc gtatgggtag agctcttctt ctgtggc

57

09067967 11601